Abstract

Characterization of potassium cation transport systems in the yeast *Zygosaccharomyces rouxii*

Potassium has become absolutely necessary cation for living cells, including yeasts, because it plays several important roles in physiological processes. Intracellular concentration of K^+ in yeasts is usually between 200 mM and 300 mM, while the external K^+ concentration is ranging from molar to micromolar. To adapt to environments with low K^+ content, yeast cells employ various K^+ high-affinity uptake systems, e.g. Trk, Hak and K^+-ATPase, that provide cells with the sufficient amount of potassium. The recent release of the complete sequence of the osmotolerant yeast *Zygosaccharomyces rouxii* genome allowed us to search homologues of the known yeast potassium uptake systems.

We have found just one gene encoding a putative potassium transporter homologous to the *S. cerevisie TRK1*. For the characterisation of transport properties and physiological roles of the product of this gene, named *ZrTRK1*, three approaches have been used. First, the IT tools serve to analyse sequence characteristics, phylogenetic relationships etc. The second approach involves cloning of the gene and its expression in a *S. cerevisiae* mutant strain lacking its own two Trk systems, characterisation of transformants' growth phenotypes and localization of the gene product in cells. The last strategy is the gene deletion in *Z. rouxii* and subsequent phenotypic characterisation of mutants. Heterologous expression of the *ZrTRK1* in *S. cerevisiae* mutant restored the ability of cells to grow at micromolar potassium concentrations. Deletion of *ZrTRK1* in *Z. rouxii* resulted in an impaired growth in media supplemented with low content of K^+. Thus this gene encodes transporter that mediates K^+ uptake. So far obtained results show that the studied gene encodes really a plasma-membrane K^+ transporter similar to the Trk transporters from *S. cerevisiae*.

(In Czech)